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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.	March 15, 2002, 03:4(	Title: US-09-652-292-1 Perfect score: 4395 Sequence: 1 gagggggtccttgccaggccattatttgtaaaaaaaaa 4395 Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0	Searched: 930621 seqs, 428662619 residues  Total number of hits satisfying chosen parameters: 1861242  Minimum DB seq length: 0  Maximum DB seq length: 2000000000	Post-processing: Minimum Match 10% Maximum Match 100% Listing first 45 summaries Database: N Genesed 1101:*		10: /51D52/gcgdtta/geneseq/geneseqn/NA1989. DAT:* 11: /51D52/gcgdtta/geneseqn/NA1990. DAT:* 12: /51D52/gcgdtta/geneseqn/NA1991. DAT:* 13: /51D52/gcgdtta/geneseqn/na1991. DAT:* 14: /51D52/gcgdtta/geneseqn/NA1992. DAT:* 15: /51D52/gcgdtta/geneseqn/NA1993. DAT:* 15: /51D52/gcgdtta/geneseqn/NA1993. DAT:* 16: /51D52/gcgdtta/geneseqn/NA1994. DAT:* 17: /51D52/gcgdtta/geneseqn/NA1995. DAT:* 17: /51D52/gcgdtta/geneseqn/NA1996. DAT:*	18: /SIDSZ/gcgdata/geneseq/geneseqn/NA1997. 19: /SIDSZ/gcgdata/geneseq/geneseqn/NA1998. 20: /SIDSZ/gcgdata/geneseq/geneseqn/NA1999. 21: /SIDSZ/gcgdata/geneseq/geneseqn/NA2000. 22: /SIDSZ/gcgdata/geneseq/geneseqn/NA2000.	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.  SUMMARIES  Result  Ouery  No. Score Match Length DB ID  Description	22 AAH50797 22 AAH13737 22 AAF17845 22 AAH62650 22 AAI57656 22 AAI57657 22 AAH92304 22 AAH02340 22 AAH02340

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                                   cancers, particularly brain cancers such as haemanglobiastoma, teratoma, haemangloma, glioblastoma, schwannoma, osteoma and pinealoma. The present sequence is a cancer-associated cDNA of the invention.
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             The present invention provides the sequences of 184 cDNA fragments are differentially expressed in cancer cell depending on the age of patient. They can be used to diagnose and identify treatments for
                                                                                                                                                                                                      Yamamoto J;
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                                                                                       Score 317.4; DB 22; Length 385; Pred. No. 5.6e-56; 0; Mismatches 6; Indels 3;
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, Otsuki T;
                                                                 Sequence 385 BP; 127 A; 61 C; 43 G; 154 T; 0 other;
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 Page 55; 82pp; English
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Sugiyama T, Wakamats
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                                                                                     Query Match 7.2%;
Best Local Similarity 97.5%;
Matches 344; Conservative C
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11-JAN-2000; 2000JP-0118776.
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Claim 28;
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The present invention describes primer sets for synthesising 5602
full-length cDNAs defined in the specification. Where a primer set
comprises: (a) an oligo-dr primer and an oligonuclectide complementary
comprises: (a) an oligo-dr primer and an oligonuclectide complementary
to the complementary strand of a polynuclectide which comprises one of
the 5602 nucleotide comprises at least 15 nuclectides; or (b) a combination
of an oligonuclectide comprising a sequence complementary to the
complementary strand of a polynuclectide which comprises a 5'-end
sequence and an oligonuclectide comprises a 3'-end sequence complementary to a
polynuclectide which comprises a 1'-end sequence. Where the
coligonuclectide comprises at least 15 nuclectides and the combination of
the 5'-end sequence3'-end sequence is selected from those defined in
the specification. The primers sets can be used in antisense therapy and
the primers are useful for synthesising polynuclectides,
particularly full-length cDNAs. The primers are also useful for the
detection and/cor diagnosis of the abnormality of the proteins encoded by
the full-length without any specialised methods. AAH03166 to AAH13628 and
AAH13631 to AAH18742 represent human cDNA sequences;
AABH3642 represent human aning a consequences.
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                                                                                                                                         Claim 8; SEQ ID 10637; 2537pp + CD ROM; English.
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Matches 258; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                             primer; detection; diagnosis; antisense therapy; gene therapy;
                                                                                                                                                                                                                                                                             The present invention provides the coding sequences and some protein sequences of proteins associated with breast cancer in humans. These sequences can be used in the diagnosis and treatment of cancers,
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                                                                                                                                                                                                                 polypeptide useful for the
breast cancer comprises at
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                                                                                                                                                                                                                                                         Claim 66; Page 189; 238pp; English
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99US-0339338.
99US-0389681.
99US-0433826.
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breast
                     Homo sapiens
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The present invention describes primer sets for synthesising 5602 (ull-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligounclectide complementary to the complementary strand of a polynuclectide which comprises one of the 5602 nuclectide sequences defined in the specification, where the coligonuclectide comprising a sequence complementary to the comprises at least 15 nuclectides; or (b) a combination of an oligonuclectide comprising a sequence complementary to the complementary strand of a polynuclectide which comprises a 3'-end sequence complementary to the complementary strand of a polynuclectide which comprises a 5'-end sequence of ligonuclectide comprises a 1'-end sequence complementary to a polynuclectide comprises a 1'-end sequence where the coligonuclectide comprises a 1'-end sequence which comprises a 1'-end sequence where the polynuclectide comprises a 1'-end sequence where the coligonuclectide comprises a 1'-end sequence where the polynuclectide comprises a 1'-end sequence of the combination of the 5'-end sequence 1'-end 1'-end
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82.3%; Pred. No. 2.7e-29;
tive 0; Mismatches 38;
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                                                                                                                                                                                                                                                                       Ota T, Isogai T, Nishikawa T, Hayashi K, S
Ishii S, Sugiyama T, Wakamatsu A, Nagai K,
                                                                   29-JUL-1999; 99JP-0248036.
27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
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nes 247; Conservative
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                                                                                                                                     Human; breast antigen; ovarian antigen; cancer; metastasis; gene therapy;
                                                                                                        Human breast or ovarian antigen genomic DNA SEQ ID NO: 300.
              AAI62650 standard; DNA; 16225 BP
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2000US-0232081
                                                                            (first entry)
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                                             AA162650;
AAI62650
ID AAI6
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Human; colorectal cancer; colorectal cancer antigen; gene therapy;
                   Human colorectal cancer antigen coding sequence SEQ ID NO: 193
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14-AUG-2000; 2
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11.JUL-2000;
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24-FEB-2000;
16-MAR-2000;
17-MAR-2000;
11-MAR-2000;
19-MAY-2000;
07-JUN-2000;
30-JUN-2000;
30-JUN-2000;
07-JUL-2000;
07-JUL-2000;
                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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             05-DEC-2000; 2000US-0251030.
05-DEC-2000; 2000US-0251988.
06-DEC-2000; 2000US-0251988.
06-DEC-2000; 2000US-0251856.
08-DEC-2000; 2000US-0251856.
08-DEC-2000; 2000US-0251868.
08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251999.
11-DEC-2000; 2000US-0251999.
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2000US-0250391
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Matches 247; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated polypeptide for treating, preventing and/or prognosing disorders related to the colon and rectum including colorectal cancers and also for testing and detection e.g. diagnosis \dot{\mathbf{r}}
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81.5%; Pred. No. 8.6e-28;
Live 0; Mismatches 41; Indels 14; Gaps
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                                                                                                                                                                                     Disclosure; SEQ ID NO: 193; 522pp + Sequence Listing; English.
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ID AAI57657 standard; DNA; 25424
                                                                              CA, Barash SC, Ruben
                                                   (HUMA-) HUMAN GENOME SCI INC
            11-DEC-2000; 2000US-0254097.
05-JAN-2001; 2001US-0259678.
08-DEC-2000; 2000US-0251990
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Matches 242; Conservative
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13-0CT-2000; 2000US-023935.
13-0CT-2000; 2000US-023935.
13-0CT-2000; 2000US-023937.
20-0CT-2000; 2000US-023937.
20-0CT-2000; 2000US-023937.
20-0CT-2000; 2000US-0241785.
20-0CT-2000; 2000US-0241787.
20-0CT-2000; 2000US-024178.
20-0CT-2000; 2000US-024179.
20-0CT-2000; 2000US-0241779.
20-0CT-2000; 2000US-024179.
20-0CT-2000; 2000US-0251186.
20-0CT-2000 

SCI INC (HUMA-) HUMAN GENOME Ç,

Ruben SM; Barash SC, Rosen

WPI; 2001-457727/49.

Isolated polypeptide for treating, preventing and/or prognosing disorders related to the colon and rectum including colorectal cancers and also for testing and detection e.g. diagnosis -

bowel disease, using a hybridization assay

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number of colorectal cancer antigens. These are shown in AAI5747-AAI57619 and AAM38569-AAM38641. These can be used in the diagnosis, prevention and freatment of cancer of the colon and/or rectum. The present sequence is a colorectal cancer antigen genomic sequence. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                          17837 TTATTTTATTTTATTTATTTATTTTTTTTTTTGAGATGGAGTCTCGCTCTGTTGCTAG 17778
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                                                 sednences of
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              ID NO: 194; 522pp + Sequence Listing; English,
                                                                                                                                                           Sequence 25424 BP; 5521 A; 6900 C; 6922 G; 6081 T; 0 other;
                                                                                                                                                                                                                                  41; Indels
                                       present invention provides the protein and coding
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Pred. No. 8.6e-28;
0; Mismatches 41
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ID AAH92304 standard; DNA; 700
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              Disclosure;
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The present invention describes a method for detecting the presence of polymorphisms associated with inflammatory bowel diseases such as ulcerative colitis and Crohn's disease. The methods can be used to detect the presence of genetic polymorphisms associated with inflammatory bowel used in this way for phencypic correlations, forensies, paternity testing, medicine and genetic analysis. The present sequence is a genetic containing a polymorphic site described in the exemplification of the
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                                                                                                                                                                                                    Score 181.8; DB 22; Length 700;
Pred. No. 4.8e-28;
0; Mismatches 46; Indels 16;
                                                                                                                                                            Sequence 700 BP; 216 A; 140 C; 192 G; 136 T; 16 other;
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Otsuki
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Sugiyama T, Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human cDNA clone (5'-primer) SEQ ID NO:794.
                      Disclosure; Page 177-178; 463pp; English.
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ID AAH03959 standard; cDNA; 883
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2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
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11-JAN-2000;
02-MAY-2000;
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complement (1565..1815)
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/note= "human C
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    ilitaria il
                                                                                                                                    The present invention describes primer sets for synthesising 5602 (ull-length cDNAs defined in the specification. Where a primer set comprises: (a) an oilgo-dr primer and an oilgouncleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oilgonucleotide comprises a least 15 nucleotides; or (b) a combination of an oilgonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oilgonucleotide comprising a sequence complementary to a polynucleotide which comprises a 1'-end sequence. Where the oilgonucleotide which comprises at least 15 nucleotides and the combination of the 5'-end sequence 3'-end sequence. The primer set as selected from those defined in the specification. The primer set as selected from those defined in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers are also useful for AAH13628 and AAH13613 to AAH13613 to AAH13613 to AAH13632 to AAH13633 to AAH13633 to AAH13633 to AAH13633 to AAH13633 to AAH13634 to AAH13632 to AAH13633 to AAH13634 to AAH13644 to AAH1
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                               Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     637 TCTCTTTATTTTTTTTTTTTTTTTTTTTTTTTTTGAGATGGAGTCTCGTTCTTGTTGCCCAG 578
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mental retardation; autism; depression; bipolar affective disorder;
hypothyroidism; OPA gene; neuropsychiatric disorder; ss.
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llarity 81.1%; Pred. No. 5.2e-28;
Conservative 0; Mismatches 42; Indels 14;
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                                                                                                            Claim 1; SEQ ID 794; 2537pp + CD ROM; English.
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WPI; 2001-318749/34
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                                                                                full-length cDNAs
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Matches 241;
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/note= "human 83018351 /*tag= s /number= 17	1 9 T	/notes 19 /notes 10 /*tag 0 /number 19	467	/note= "human 997310104 /*tag= w	/number= 21 /note= "human 1053010757 /ttag= x	/number= 22 /note= "human 1093311077 /*tag= y		12 a	/number= 25 /note= "human 1231712492 /ttag= ab	/number= 2b /note= "human 1267212851 /*tag= ac	/number= 2/ /note= *human 1418714258 /*tag= ad /number= 28	- դ 14	/number= 29 /note= "human 1501415175 /*tag= af /number= 30	fo.		Z / B	human 7492 aj 34	human
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14; Gaps Query Match
4.1%; Score 181.8; DB 21; Length 54548;
Best Local Similarity 74.2%; Pred. No. 2.4e-27;
Matches 262; Conservative 0; Mismatches 77; Indels 14; /\*tag= au /note= "probable NL-3 promoter" // Unducer = 20372..20590
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// number = 40
// note = "human OPA promoter"
23283..23505
// tag = aq
// number = 41
// note = "human OPA promoter"
23878..24018 /\*tag= ar /number= 42 /note= "human OPA promoter" 24531..24612 /number= 43 /note= "human OPA promoter" 24823..25096 /number= 44 /note= "human OPA promoter" 26123..26275 'number- 35 \*tag= at promoter exon exon exon exon exon exon exon exon exon q ŏ ò g ŏ q ò

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standard; DNA; 162025

RESULT 11

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12-JUN-2001
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                                                                                            human; genetic marker; disease; infection;
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                                                                                                                                                                                                                                                                                                         Chiu
                                                                                                                                                                                                                                                                                                                                                                 Producing a database for identifying polymorphic genetic markers, comprises obtaining data relating to members of a healthy population and entering the information into a database -
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Pred. No. 5.3e-27;
0; Mismatches 40;
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                                                                                                                                                                                                                                                                                                                                                                                                              Example 3; Page 241-288; 304pp; English.
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 DNA; 161425
                                                                     Human AKAP10 gene SEQ 1D NO:
                                                                                           polymorphism; SNP;
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ilarity 81.6%;
Conservative (
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AAH02340 standard;
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Best Local Similarity
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                                                                                                                              Homo saptens.
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The present invention provides a database of human samples obtained from healthy individuals which can be used to identify polymorphic genetic markers. Data obtained for the database can be used to sort the samples by parameters such as age, sex and ethnicity. This is useful in linking markers with diseases, susceptibility to infection and drug responses. The present sequence was used in an assay to demonstrate the uses of the database of the invention.
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                                                                                                      Database; polymorphism; SNP; human; genetic marker; disease; infection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tttgtatttttagtagagacagggtttcaccatgttggccaggccggtcttgaactcctg
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Pred. No. 5.3e-27;
0; Mismatches 40;
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al Similarity 81.6%;
239; Conservative
                                                   Human AKAP10 gene SEQ ID NO:
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10-JUL-2000; 2000US-0217251.
10-JUL-2000; 2000US-0217658.
19-SEP-2000; 2000US-0663968.
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(first entry)
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                                       420 ЫНИЧИНИЯНИЯНИЯНИЯНИЯНИЯНИЯНИЯТААССИЯНИЯНИЯНИЯНИЯНИЯНИЯНИЯНИЯНИЯНИЯНИЯ 361
                                                                                                                                                The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic
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17-MAR-2000; 2000US-0190259
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Local Similarity 0.7%; Pred. No. 8.5e-;
es 5; Conservative 526; Mismatches
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                                  Sequence 936 BP; 4 A; 144 C; 7 G; 5 T; 776 other
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Electron-transfer group; ETM; mismatch; genotyping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 936 BP; 5 A; 142 C; 7 G; 6 T; 776 other;
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                                                                                                                                                                                                                                                                                                                                                                              (CLIN-) CLINICAL MICRO SENSORS INC
                                                                                                                                                                                                                                            26-JUL-2000; 2000WO-US20476
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                            gene expression; ss
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4295	4292 aaagattctgtaagaattaattggctatatgggaatttaggatagaatatttacaataaag 4351 	4351
4352	4352 agtatttacaataaagagtttgttattattgtaaaaaaaa	